

FT230" E2E4E660

Human 33410

Carboxylesterase Domain

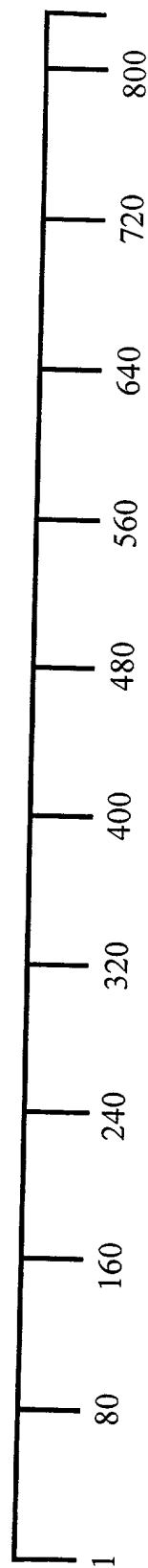
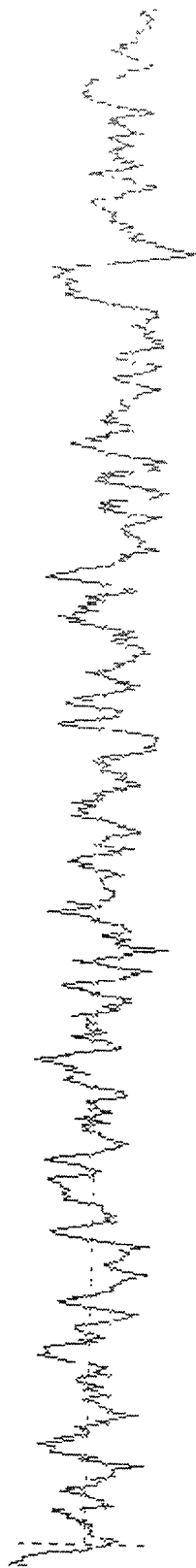


FIG. 1

Coesterase: domain 1 of 1, from 42 to 601: score 440.0, E = 2.1e-128	
	*->llVatnnVlcGkvrGvnektDn...geqsvysFlGIPYAePPVGnLR
Fbh33410FL	42 ++V+t + G vrGv++ ++n+ g +v FlG+PYA PP+G R PVVNTAY---GRVRGVRRELNNeilG--PVVQFLGVYPYATPPLGARR 83
Fbh33410FL	84 FkaPqPYkepWsdvldAtkyppsClQdddfgfslsdLKva.lkmlslgwn F +P+ + W +v+++At+ pp+C+Q+ g +++ +ml+ ++ FQPPEA-PASWPGVRNATTLPPACQNLH-G-----ALpAImLPVWFT 124
Fbh33410FL	125 klvg.....lklSEdCLYLNVytPkntkpns..... ++ + +sEdCLYLN y+p + p +++++ + +++++ + DNLEaaatyvQNQSEdCLYLNLYVPTEDGPLTKkrdeatlnppdttdirdp 174
Fbh33410FL	175 .klPvmVwIhGGGFmfGsgHslplslYdgeslaregnVivVsiNYRLGpl +k Pvm + hGG +m G+g + dg+ la+ gnViv ++NYRLG+l gKKPVMLFLHGGSYMEGTG-----NMFDGSVLAAyGNVIVATLNYRLGVL 219
Fbh33410FL	220 GFLstgddklpgsGNyGLlDQrlALKWVqdNIaaFGGDPnsVTifGeSAG GFLstgd + GNYGLlDQ+ AL+W +NIa+FGGDP+++TifG AG GFLSTGDQAAK--GNyGLLDQlQALRWLSENIAHFGGDPERITIFGSGAG 267
Fbh33410FL	268 aaSVsl1111sngGDNppsskgLFhRAIsqSGsalspwaiqsesnargrak a+ V ll+ls +s+gLf++AI qSG+a+s w++ + ++ ASCVNLLILS-----HHSEGLFQKAIAQSGTAISSWSVNYQP--LKYTR 309
Fbh33410FL	310 elarllGCnetssselldCLRsksaeelLeatrsfllfeyvpflplflaF la+++GC++++s+e ++CLR+k+++eL++ +++++y + + LLAAKVGCDREDSAEAVECLRRKPSRELVDQDV--QPARYHIAFG----- 352
Fbh33410FL	353 gPvvDGDdapeafipedPeelikeGkfadvPyliGvtkdEGgyfaamlln PvvDGDd ++p+dPe+l +G f + ++liGv++ EG+ f + -PVVDGD-----VVPDDPEILMQQGEFLNYDMLIGVNQGEGLKFV----E 392
Fbh33410FL	393 asskgedelkketnpdvwllellkyllfyasealnikdMddladvlekYp +s+ ted ++ ++ + ++ l++ +e + d l +++++ Y+ DSAESEDGVSASAFDF-TVSNFVDNLYGYPEGK-----DVLRETIKFMYT 436
Fbh33410FL	437 gdvdffsvesrkpnlqdmldtDl1FkcptrvaadhakhggsPvYaYvfdh +++d+ e r++ l+ +tD+ + p +va ++ +++ +sPvY+Y f h DWADRDNGEMRRKTLALFTDhQWVAP-AVATAKLHADYQSPVYFYTFYH 485
Fbh33410FL	486 pasfgigQflakrvdpeffgavHgdEiffvFgnpllikeglyka...teee + + +pe+ a HgdE+++vFg+p + ++ + + ++ + HCQ-----AEGRPEWADAAGDELpYVFGVPMVGATDLFFCnfsKND 527
Fbh33410FL	528 eksssktmmnywanFAktGnPn....ngts.....nglvvWpkytse +++s ++m yw+nFAktG+pnn+ + +t +++++++vvW k++s+ VMLS-AVVMTYWTNFAKTGDPNqpvpQDTKfihtkpnrFEVVWSKFNSK 576
Fbh33410FL	577 eqkYsl1111ttitaqklkardprkvlcnfw<-* e +l+i l+ +++++a++ +fw EKQ-YLHIGLKPRVRDNYRANK-----VAFW 601

Figure 2

CLUSTAL W (1.74) multiple sequence alignment

Fbh33410FL
ratNL2 =
rat neu kgn 2

MWLLALCLVGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVGRVRELN
MWLLALCLVGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVGRVRELN

Fbh33410FL
ratNL2

EILGPVVQFLGVPIATPPLGARRFQPPEAPASWPGVRNATTLPPACQNLHGALPAIMLP
EILGPVVQFLGVPIATPPLGARRFQPPEAPASWPGVRNATTLPPACQNLHGALPAIMLP

Fbh33410FL
ratNL2

VWFTDNLEAAATYVQNQSEDCLYLNLYVPTEDGPLTKKRDEATLNPPDIDIRDPGKKPVM
VWFTDNLEAAATYVQNQSEDCLYLNLYVPTEDGPLTKKRDEATLNPPDIDIRDSGKKPVM

Fbh33410FL
ratNL2

LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNRYRLGVLGFLSTGDQAAKGNYGLLDQIQ
LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNRYRLGVLGFLSTGDQAAKGNYGLLDQIQ

Fbh33410FL
ratNL2

ALRWLSENIHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIQSGTAISSWSV
ALRWLSENIHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIQSGTAISSWSV

Fbh33410FL
ratNL2

NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
NYQPLKYTRLLAAKVGCDREDSTEAVECLRRKSSRELVDQDVQPARYHIAFGPVVDGDVV

Fbh33410FL
ratNL2

PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY

Fbh33410FL
ratNL2

PEGKDVLRETIKFMYTDWADRDNEMRRKTLLALFTDHQWVAPAVATAKLHADYQSPVYF
PEGKDVLRETIKFMYTDWADRDNEMRRKTLLALFTDHQWVAPAVATAKLHADYQSPVYF

Fbh33410FL
ratNL2

YTFYHHCQAEGRPEWADAAGHDELPHYVFGVPMVGATDLFPCNFSKNDVMLS AVVMTYWTN
YTFYHHCQAEGRPEWADAAGHDELPHYVFGVPMVGATDLFPCNFSKNDVMLS AVVMTYWTN

Fbh33410FL
ratNL2

FAKTGDPNQVPVQDTKFIHTKPNRFEEVWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
FAKTGDPNQVPVQDTKFIHTKPNRFEEVWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF

Fbh33410FL
ratNL2

WLELVPHLHNLHTELF TTTTTLPPYATRWPPRPP-AGAPGTRRPPPPATLPPEPEPEPGP
WLELVPHLHNLHTELF TTTTTLPPYATRWPPRTPGPGTSGTRRPPPPATLPPESDIDLGP

Fbh33410FL
ratNL2

RAYDRFPGDSRDYSTELSVTVAVGASLLFLNIIAFAALY YKDRRQELRCRRLSPPGGSG
RAYDRFPGDSRDYSTELSVTVAVGASLLFLNIIAFAALY YKDRRQELRCRRLSPPGGSG

Fbh33410FL
ratNL2

SGVPGGGPLLPAAGREL PEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDD
SGVPGGGPLLPTAGREL PEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDD

Fbh33410FL
ratNL2

VPLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPFPPTATSHNNTLPHPHSTTRV
VPLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPFPPTATSHNNTLPHPHSTTRV

Figure 3

CLUSTAL W (1.74) multiple sequence alignment

```

Fbh33410FL      MWLLALCLVGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVRGVRRELNN
KIAA1366      -----

Fbh33410FL      EILGPVVQFLGVPYATPPLGARRFQPPEAPASWPGVRNATTLPPACPQNLHGALPAIMLP
KIAA1366      -----

Fbh33410FL      VWFTDNLEAAATYVQNQSEDCLYLNLVPTEDGPLTKKRDEATLNPPDTDIRDPGKKPVM
KIAA1366      -----

Fbh33410FL      LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNYRLGVLGFLSTGDQAAKGNYGLLDQIQ
KIAA1366      -----

Fbh33410FL      ALRWLSENI AHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAI AQSGTAISSWSV
KIAA1366      -----KAIAQSGTAISSWSV
                        *****

Fbh33410FL      NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
KIAA1366      NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
                        *****

Fbh33410FL      PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
KIAA1366      PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
                        *****

Fbh33410FL      PEGKDVLRETIKFMYTDWADRDNGEMRRKTL LALFTDHQWVAPAVATAKLHADYQSPVYF
KIAA1366      PEGKDVLRETIKFMYTDWADRDNGEMRRKTL LALFTDHQWVAPAVATAKLHADYQSPVYF
                        *****

Fbh33410FL      YTFYHHCQAEGRPEWADAAHGDELPYVFGVPMVGATDLFPCNFSKNDVMLS AVVM TYWTN
KIAA1366      YTFYHHCQAEGRPEWADAAHGDELPYVFGVPMVGATDLFPCNFSKNDVMLS AVVM TYWTN
                        *****

Fbh33410FL      FAKTGDPNQVPVQDTKFIHTKPNRFEEVWWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
KIAA1366      FAKTGDPNQVPVQDTKFIHTKPNRFEEVWWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
                        *****

Fbh33410FL      WLELVPHLHNLHTELF TTTTTRLPPYATRWPPRPPAGAPGTRRPPPPATLPPEPEPEPGPR
KIAA1366      WLELVPHLHNLHTELF TTTTTRLPPYATRWPPRPPAGAPGTRRPPPPATLPPEPEPEPGPR
                        *****

Fbh33410FL      AYDRFPGDSRDYSTELSVTVAVGASLLFLN ILAFAALY YKRDRRQELRCRRLSPPGGSGS
KIAA1366      AYDRFPGDSRDYSTELSVTVAVGASLLFLN ILAFAALY YKRDRRQELRCRRLSPPGGSGS
                        *****

Fbh33410FL      GVPGGGPLLPAAGRELPPEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDDV
KIAA1366      GVPGGGPLLPAAGRELPPEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDDV
                        *****

Fbh33410FL      PLLAPGALTLLPSGLGPPPPPPPPSLHPFGFPFPPPPPTATSHNNTLPHPHSTTRV
KIAA1366      PLLAPGALTLLPSGLGPPPPPPPPSLHPFGFPFPPPPPTATSHNNTLPHPHSTTRV
                        *****

```

Figure 4